



SEQUENCE LISTING

<110> Nicholson, Geoffrey

<120> METHOD OF TREATMENT AND AGENTS USEFUL
FOR SAME

<130> DAVI103.001AUS

<140> 09/632,074

<141> 2000-08-02

<150> AU/PQ/1999

<151> 1999-08-03

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 504

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)... (504)

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atg cat tgg gga acc ctg tgc gga ttc ttg tgg ctt tgg ccc tat ctt 48
Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
1 5 10 15

ttc tat gtc caa gct gtg ccc atc caa aaa gtc caa gat gac acc aaa 96
Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
20 25 30

acc ctc atc aag aca att gtc acc agg atc aat gac att tca cac acg 144
Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
35 40 45

cag tca gtc tcc tcc aaa cag aaa gtc acc ggt ttg gac ttc att cct 192
Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
50 55 60

ggg ctc cac ccc atc ctg acc tta tcc aag atg gac cag aca ctg gca 240
Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
65 70 75 80

gtc tac caa cag atc ctc acc agt atg cct tcc aga aac gtg atc caa 288
Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
85 90 95

ata tcc aac gac ctg gag aac ctc cgg gat ctt ctt cac gtg ctg gcc 336

Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
 100 105 110

ttc tct aag agc tgc cac ttg ccc tgg gcc agt ggc ctg gag acc ttg 384
 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
 115 120 125

gac agc ctg ggg ggt gtc ctg gaa gct tca ggc tac tcc aca gag gtg 432
 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
 130 135 140

gtg gcc ctg agc agg ctg cag ggg tct ctg cag gac atg ctg tgg cag 480
 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
 145 150 155 160

ctg gac ctc agc cct ggg tgc tga 504
 Leu Asp Leu Ser Pro Gly Cys *
 165

<210> 2
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
 1 5 10 15
 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
 20 25 30
 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
 35 40 45
 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
 50 55 60
 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
 65 70 75 80
 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
 85 90 95
 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
 100 105 110
 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
 115 120 125
 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
 130 135 140
 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
 145 150 155 160
 Leu Asp Leu Ser Pro Gly Cys
 165

<210> 3
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
<223> GAPDH forward primer.

<400> 3
cagtcagccg catcttcttt tg 22

<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> GAPDH backward primer.

<400> 4
tggttcacac ccatgacgaa c 21

<210> 5
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> OPG forward primer.

<400> 5
gtacgtcaag caggagtga atc 23

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> OPG backward primer.

<400> 6
ttcttgtgag ctgtgttgcc g 21

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> RANK forward primer.

<400> 7
ttaagccagt gcttcacggg 20

B4
Cont.

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> RANK backward primer.

<400> 8
acgtagacca cgatgatgtc gc

22